



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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Applicant : Chappell et al.
Serial No. : 09/893,820
Filed : June 28, 2001
Title : SYNTHASES

Art Unit : 1631
Examiner : L. Clow

JUN 24 2002

TECH CENTER 1600/2900

Commissioner for Patents
Washington, D.C. 20231

PRELIMINARY AMENDMENT

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Prior to examination, please amend the application as follows:

In the Specification:

Please replace the paragraph on page 1, lines 11-13, with the following paragraph:

--This work was supported, in part, with funding from NIH (GM54029 and GM07240) and NSF (IBW-9408152). Therefore, the United States Federal Government may have certain rights in the invention.--

Please replace the paragraph on page 13, lines 5-8, with the following amended paragraph:

--Figure 1. Schematic representation of tobacco 5-epi-aristolochene synthase (TEAS) with bound farnesyl hydroxyphosphonate (FHP), prepared using the RIBBONS software program of Carson, M. and Bugg, C., J. Mol. Graphics 4:121 (1986). Cylinders 1-8 and A represent α -helices in the NH₂-terminal domain; cylinders C, D, D1, D2, E, F, G1, G2, H1, H2, H3, I and α -1 represent α -helices in the COOH-terminal domain.--

Please replace the paragraph on page 26, lines 14-23, with the following amended paragraph:

CERTIFICATE OF MAILING BY FIRST CLASS MAIL

I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.

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--As exemplified by TEAS, terpene synthases of the present invention can have a first domain segment comprising helices A and C (an A-C loop), and a second domain comprising helices J and K (a J-K loop) (Figure 1). The ordering of these loops upon substrate binding results in a closed, solvent-inaccessible active site pocket. As the J-K loop becomes ordered, a lid-type structure is formed that clamps down over the active site entrance in the presence of substrate and an extended aromatic patch deep within the active site pocket is formed. As the A-C loop becomes ordered, it translates inward toward the active site, positioning certain R groups in this loop at or near the active site. Thus, substrate binding to the active site results in a change in protein conformation.--